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GenCore version 5.1.6
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OM protein - protein search, using sw model

2, 2004, 19:30:36; Search time 55 Seconds June Run on:

(without alignments) 498.311 Million cell updates/sec

506 1 MIQLTPLQLFKNLSDETRLG......PSWAAQIIEQAWLSQQDDVQ US-10-676-296-2_COPY_1_97 Perfect score: Sequence: Title:

97

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* 1: geneseqp1980s:* geneseqp1980s:* Database

genesequi90s:* genesequ200s:* genesequ2001s:* genesequ2002s:* genesequ2003as:* genesequ2003as:* genesequ2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Abu63440 E. coli A		Abul5462 Protein e	Abg24942 Novel hum	Abu49785 Protein e	Abu27992 Protein e	Abu27449 Protein e	Abg18368 Novel hum	Abu41107 Protein e	Abu40241 Protein e		•	Abu49297 Protein e		Ada35167 Acinetoba	Abu36828 Protein e	Abu34403 Protein e	Abb48872 Listeria	Abu33098 Protein e	Abul7506 Protein e	Abu19574 Protein e	Abu24703 Protein e	ő	Aab79020 C. glutam	Aag92802 C glutami
	ID	ABU63440	ABU31952	ABU15462	ABG24942	ABU49785	ABU27992	ABU27449	ABG18368	ABU41107	ABU40241	ABU38444	ADA36925	ABU49297	ABU16869	ADA35167	ABU36828	ABU34403	ABB48872	ABU33098	ABU17506	ABU19574	ABU24703	AAB76789	AAB79020	AAG92802
	DB	9	9			9	_	9	•	9	_	9		-	_	9				9				4	4	4
	Length DB	117	109	117	973	113	106	111	576	111	115	116	110	113	109	116	126	126	111	111	101	107	107	123	123	129
æ	거석	100.0	85.2	81.8	81.8	78.9	0.69	64.6	61.7	59.9	55.7	52.6	48.4	45.1	44.9	44.9	29.8	29.8	26.9	26.9	26.7	26.4	25.8	25.4	25.4	25.4
	Score	206	431	414	414	399	349	327	312	303	282	266	245	228	227	227	151	151	136	136	135	133.5	130.5	128.5	128.5	128.5
	ισ C		7	3	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

B. faeciu	Protein e	Staphyloc	Protein e	Protein e	Protein e	Putative	Protein e	Protein e	Protein e	Staphyloc	Protein e	Staphyloc	E. faeciu	Protein e	Streptoco	Putative	Protein e	Protein e	Streptoco	
Adc97044	Abu25960	Abp38051	Abu28998	Abu24235	Abu42712	Aab96258	Abu22386	Abu19373	Abu43995	Abp38139	Abu34202	Abp39152	Adc97456	Abu46886	Abp29628	Aab96781	Abu25260	Abu42450	Abp30704	
ADC97044	ABU25960	ABP38051	ABU28998	ABU24235	ABU42712	AAB96258	ABU22386	ABU19373	ABU43995	ABP38139	ABU34202	ABP39152	ADC97456	ABU46886	ABP29628	AAB96781	ABU25260	ABU42450	ABP30704	
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105	89	127	95	122	104	118	115	116	105	110	134	117	120	112	122	134	121	104	122	
25.2	25.0	24.9	24.6	24.1	24.0	23.8	23.6	23.1	22.9	22.8	22.8	22.7	22.7	22.3	22.3	22.2	21.9	21.8	21.8	
127.5	126.5	126	124.5	122	121.5	120.5	119.5	117	116	115.5	115.5	115	115	113	113	112.5	111	110.5	110.5	
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1 ABU63440

ABU63440 standard; protein; 117 AA.

ABU63440;

(first entry) 10-OCT-2003

E. coli ArsR protein.

Arsk; arsenic resistance operon; biosensor; codon optimisation; arsenic.

Escherichia coli.

 97 /note= "Thus region is specifically claimed in claim 33" Location/Qualifiers Region

22-MAY-2003.

US2003096275-A1.

15-AUG-2002; 2002US-00222952.

20-AUG-2001; 2001US-0313714P. (LAIN/) LAING L G.

Laing LG;

WPI; 2003-576876/54. N-PSDB; ACD28583. New system comprising isolated protein and nucleic acid, and a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte, useful for detecting the presence of analyte in a sample.

Claim 32; Page 16; 36pp; English.

The invention relates to a new system (biosensor) for detecting the presence of analyte in a sample comprising: (1) an isolated protein that specifically binds the analyte; (2) an isolated nucleic acid containing a specific binding sequence that is bound specifically by the protein; and (3) a detection system that indicates a change in binding of the protein to the nucleic acid in the presence of the analyte. Also included are a biosensor device for detecting the presence of an analyte in a sample, detecting the presence of an analyte in a sample,

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     E. coli) protein comprising an identical to amino acids 1-97 of
part of the arsenic resistance operon of E. coli) protein comprising an amino acid sequence that is at least 90% identical to amino acids 1-97 of the ArsR sequence appearing as ABUG3440 binding to a nucleic acid sequence comprising oliquonucleotides appearing as ACD28584-ACD28591. The system is useful for detecting the presence of analyte in a sample. The present sequence is the E. coli ArsR protein (encoded by a codon optimised DNA) used in the biosensor of the invention to detect arsenic
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0
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                                                                                                                                                                                         ; Score 506; DB 6;
; Pred. No. 5.8e-54;
0; Mismatches 0;
                                                                                                                                                                                                 100.0%;
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Matches 97; Conservative
                                                                                                                                                             Sequence 117 AA;
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ABU31952 standard; protein; 109 ABU31952; RESULT 2 ABU31952

61 LDRKOGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97

LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ

g 8

7

Antisense; prokaryotic essential gene; cell proliferation; drug design. Protein encoded by Prokaryotic essential gene #17479.

(first entry)

19-JUN-2003

WO200277183-A2 03-OCT-2002 21-MAR-2002; 2002WO-US009107.

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 2002US-00072851. 2002US-0362699P. 06-MAR-2002; 08-FEB-2002;

ELITRA PHARM INC. (ELIT-) Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, 'n, Wang |

2003-029926/02. N-PSDB; ACA35822

screening New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

21-WAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00372851. 06-WAR-2002; 2002US-0362699P.

Claim 25; SEQ ID NO 59876; 1766pp; English.

the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (3) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for

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proliferation; // learning a compound unar intimizers are controlled to the gene product or that has an activity against a biological pathway controlled for proliferation, or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits cellular proliferation; (8) to pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an corganism acts; (9) manufacturing an antibictic; (10) profiling a compound; activity; (11) a culture comprising strains in which the gene or compound; or its gene or underexpressed; (12) determining the extent product is overexpressed or underexpressed; (12) determining the extent product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of the which expenditely or compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for controlleration of the strains for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, craquired for proliferation in cells other than S. aureus, S. typhimurium, the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
identifying a compound that influences the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #989.
                                                                                                                                                                                                                                                                                                                                                                                                   Score 431; DB 6; L6
Pred. No. 8.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 DRKOGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 85.2%; Score 431; DE Similarity 83.3%; Pred. No. 8.5e 80; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
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        proliferation; (7)
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 109 AA;
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ABU15462
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, WPI; 2003-029926/02. N-PSDB; ACA19332. Wang L, Wall D,

23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC

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The invention relates to an isolated mucleic acid compileration where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated are:

onlypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway to proliferation, or that inhibits proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or which he test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocic; (10) profiling a product is overexpressed or underexpressed; (12) determining the extent or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecic acids are quired for cellular proliferation to isolate candidate molecic acids are quired for cellular proliferation to isolate candidate molecic acids are quired for cellular proliferation to isolate candidate molecic acids are quired.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                     any
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isolate candidate molecules for rational drug discovery programs
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                                                                                                     The invention relates to an isolated nucleic acid comprising
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80.9%; Pred. No. 1.1e-42;
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                                                  Claim 25; SEQ ID NO 43386; 1766pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG24942 standard; protein; 973 AA
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Les 76; Conservative
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging complement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in financial capanists, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and aming a sold sequences. Abgoloulo-Abgolary respessent novel human diagnostic aming acid sequences. Abgoloulo-Abgolary respessent novel human diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 414; DB 4; Length 973;
80.9%; Pred. No. 1.7e-41;
tive 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #35312.
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                                                                                                                                                                                                                                                                       Claim 20; SEQ ID NO 55301; 103pp; English.
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                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.9%
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                             WPI; 2001-639362/73.
N-PSDB; AAS89129.
                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 973 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200277183-A2.
                                                                                                                                                                                                                                    biodiversity
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Interobacter cloacae

WO200277183-A2. 03-OCT-2002

Haselbeck R,

Protein encoded by Prokaryotic essential gene #13519.

19-JUN-2003 (first entry)

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06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                 ELITRA PHARM INC.
21-MAR-2001;
06-SEP-2001;
           36-MAR-2002;
                 ELIT-)
                       ijά
                       Wang
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The invention relates to an isolated nucleic acid compiliating of the following the following any one of the mucleic acid inhibits proliferation of a cell. Also included are:

of the mucleic acid inhibits proliferation of a cell. Also included are:

of the mucleic acid inhibits proliferation of a cell. Also included are:

concoding a polypeptide whose expression is inhibited by the antisense

nucleic acid; (2) a host cell containing the vector; (3) an isolated

concoding a polypeptide or its fragment whose expression is inhibited by the antisense

controlleration or the activity of a gene in an operon required for the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

controlleration; (7) identifying a compound that influences the activity of proliferation, or that has an activity against a biological pathway to proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the est compound that inhibits proliferation of a compound that inhibits proliferation of compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the controlleration of an organism. The antisense nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, required for proliferation in cells other than S. aureus, S. typhimurium, control or control or screening for sequence and sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this entered for mat directly from Mileone.
                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      one of
Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated nucleic acid comprising any
          Ohlsen KL,
Forsyth RA,
                                                                    Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 77709; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                    Malone C,
Carr GJ,
                          Zamudio C,
Trawick JD,
                                                                                                                                                                             2003-029926/02
                                                                                                                                                                                                                                 N-PSDB; ACA53655
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screening

New antisense nucleic acids, useful for identifying proteins or scre for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 55916; 1766pp; English.

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Wang L, Wall D,

WPI: 2003-029926/02.

N-PSDB; ACA31862

06-SEP-2001; 2011US-00948993. 25-OCT-2001; 2011US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD,

21-MAR-2002; 2002WO-US009107. 21-MAR-2001; 2001US-00815242.

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                                                                       1 MIQITPLQLFKNISDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGIL
                                                                                        1 MTILTPLQLFKNLSDETRINIILLKASGELCVCELCHRINEAQPKISRHLAMIRESGLL
                                               Gaps
                                               0;
                   78.9%; Score 399; DB 6; Length 113; 76.0%; Pred. No. 7.6e-41; cive 13; Mismatches 10; Indels
                                                                                                                                             LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDV 96
                                      Local Similarity 76.0
Sequence 113 AA;
                                                                                                                                  61
                       Query Match
                                                     Matches
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Gaps
                                                                                                                                                         0,
                                                                                                                                                     Length 106;
                                                                                                                                                         Indels
                                                                                                                                                   69.0%; Score 349; DB 6; Lk
69.8%; Pred. No. 9.6e-35;
w.ematrohes 9;
                                                                                                                                                     Query Match
Best Local Similarity 69.8#
Matches 60; Conservative
                                                                                                                                                 Sequence 106 AA;
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present sequence is encoded by one of

drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium K. pneumoniae or P. aeruginosa. The present sequence is encoded by one patent encounted parts of the printed specification, but was obtained in electronic form at directly from WIPO at fire, int/pub/published_pct_sequences

typhimurium

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The invention relates to an isolated nucleic acid comprising any one of the forly antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

Co of the nucleic acid inhibits proliferation of a cell. Also included are:

Co of the nucleic acid inhibits proliferation is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated are:

Co polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway in which a proliferation. The inhibits cellular proliferation of an identifying a gene required for cellular proliferation or the biological contains a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture computation of product is overexpressed or underexpressed; (12) determining the extent organism acts; (9) identifying the target of a compound that inhibits the gene or which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits to compound the proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism. The antisense nucleic acids are useful for each allular proliferation to isolate candidate molecules for rational activity is a solation or antisense in a conditional activity and antisense in a conditional activity and a solation or antisense mucleic acids are useful for a conditional activity and an organism.

ABU27992 standard; protein; 106

ABU27992;

ABU27992 ID ABU2 XX AC ABU2 XX

RESULT 6

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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
contisense nucleic acid; (4) an activity of agene in an operon required for
proliferation, or that has an activity against a biological pathway
contentifying a gene or which the test compound that inhibits cellular proliferation of
the gene or which he test compound that inhibits proliferation of
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
corganism acts; (11) a culture comprising strains in which the gene
corpound; a coverxpressed or underexpressed; (12) determining the extent
corganism; or (13) identifying the target of a compound that inhibits the
contents; overxpressed or underexpressed; (12) determining the
contents; or (13) identifying the target of a compound that inhibits the
contents; or (13) identifying the target of a compound
content or organism. The antisense nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #12976.
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 55373; 1766pp; English.
                                                                    64 KQGKWVHYRLSPHIPSWAAQIIEQAW 89
                                                                                            REGKWVHYRLSPNMPAWAAVVIDNSW 87
                                                                                                                                                                                                                       ABU27449 standard; protein; 111 AA.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-CCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
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                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacter cloacae.
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Trawick JD,
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Wall D,
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required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                     89
                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                 9 LFKNLSDETRIGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKW
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                     ;
                                                                                                                                                                Length 111;
                                                                                                                                                                                                     10; Indels
                                                                                                                                                              64.6%; Score 327; DB 6; 70.4%; Pred. No. 5.1e-32; ive 14; Mismatches 10.
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                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human diagnostic protein #18359.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG18368 standard; protein; 576 AA.
                                                                                                                                                                                                                                                                                                              69 VHYRLSPHIPSWAAQIIEQAW 89
                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002 (first entry)
                                                                                                                                                       Query Match
Best Local Similarity 70.4%
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                                                                                                                                  Sequence 111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG18368;
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 LCVCDLCTALDQSQPKISRHLALLRESGLLLDRKQGKWVHYRLSPHIPAWAAKIIDEAWR 131
diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 LCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKWVHYRLSPHIPSWAAQIIBQAWL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                     Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by Prokaryotic essential gene #26634.
                                                                                                                                                                                                                                                                                                                                                        61.7%; Score 312; DB 4; 82.1%; Pred. No. 2.9e-29;
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU41107 standard; protein; 111 AA.
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Carr GJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                            55; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 CEÓEKVO 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 SOQDDVQ 97
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                    Sequence 576 AA;
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Wall D,
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ABU41107
ABU41107
ABU41107
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proliferation or the activity or a gene in an operon required for the proliferation, (7) identifying a compound that influences the activity of the proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that his an activity against a biological pathway contained for proliferation, or that inhibits cellular proliferation or the biological identifying a gene required for cellular proliferation or the biological or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or oppound is overexpressed or underexpressed, (12) determining the extent of the virial product is overexpressed or underexpressed, (12) determining the extent or object of the strains is present in a culture or collection of the strains is present in a culture or collection of the strains. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimmrium, required for proliferation in cells other than S. aureus, S. typhimmrium, required for proliferation in cells other than S. aureus, S. typhimmrium, center the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LTPLOLFKNISDETRIGIVILIREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
proliferation or the activity of a gene in an operon required for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 111;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #25768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 303; DB 6;
; Pred. No. 4.5e-29;
13; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 KOGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KQGKWVHYRLSPVLLPWVKSIIDITYTTEKNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU40241 standard; protein; 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 63.4%;
Matches 59; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 111 AA;
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Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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The invention relates to an isolated nucleic acid comprising any one of the invention relates to an isolated nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proinferation of a cell. Also included are:

(1) a vector comprising a proinferation of a cell. Also included are:

(2) a vector comprising a promoter operably linked to the mucleic acid denoted acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide, (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or the product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits proliferation of strains; or (13) identifying the target of a compound that inhibits collection of strains; or (13) identifying the target of a compound that inhibits collection of strains; or capacing proteins or screening for homologous nucleic acids required for cellular proliferation to stolate enadidate molecules for tational acids are defined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LIPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ITPPDVFKSLSDETRARATLLIASLGELCVCELMCALNDSQFKISRHLAQLRSNGMLLDR 61
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for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.7%; Score 282; DB 6; Length 115; 54.3%; Pred. No. 1.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #23971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 KQGKWVHYRLSPHIPSWAAQIIE-----QAWLS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :||:||:||:||:
62 RQGQWVYYRLNPELPSWVHEMLQVTLQANSQWLA 95
                                                                                Claim 25; SEQ ID NO 68165; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU38444 standard; protein; 116 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 115 AA;
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ABU38444
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The invention relates to an isolated nucleic actual compliancy of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid inhibits proliferation is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound activity, all a culture compound that inhibits in which the strains is present in a culture or collection of an organism. The antisense mucleic acids are useful for proliferation of an organism. The antisense mucleic acids are useful for collular proliferation of an organism. The antisense mucleic acids required contents for proliferation of an organism. The antisense mucleic acids required contents for proliferation of an organism. The antisense mucleic acids required contents for proliferation of the strains of the stra
                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                      Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.6%; Score 266; DB 6; Best Local Similarity 51.6%; Pred. No. 1.7e-24; Matches 48; Conservative 22; Mismatches 23.
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                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                     claim 25; SEQ ID NO 66368; 1766pp; English.
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                                                                                                                                                                              Malone C,
                                                                                                                                                                                                   Carr GJ,
                     25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                           (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                              Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                         WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                    N-PSDB; ACA42314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 116 AA;
06-SEP-2001;
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                                                                                                                                                                              Wang L,
Wall D,
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     EXXXE
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98US-0088701P. 99US-00328352

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Protein encoded by Prokaryotic essential gene #34824
                                                                                                                                                                          Example; SEQ ID NO 8212; 328pp; English.
     Acinetobacter baumannii protein #4086.
                                                                                                                                                                                                                                                                                                                  RKQGKWVHYRLSPHIPSWAAQIIE 86
                                                                                                                                                                                                                                                                                                                          |:|:||:|::
RRQSQWVYYSINQQLPAWCFEILD
                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                             ABU49297 standard; protein; 113
                                                                                                                                                                                                                                                                              45; Conservative
                                   Acinetobacter baumannii
                                                                                                                         WPI; 2003-576092/54.
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                             Breton G, Bush D;
                                                                                                                                N-PSDB; ADA32799.
                                                                                                                                                                                                                                                      Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200277183-A2
                                                                         04-JUN-1999;
                                                                                    09-JUN-1998;
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                                                US6562958-B1
                                                            L3-MAY-2003
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                                                                                                                                                                plants.
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The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a promoter operably linked to the nucleic acid conclains a polypeptide whose expression is inhibited by the antisense contisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the actising the polypeptide; (5) producing the polypeptide; (6) an isolated for the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or proliferation or the activity of a gene in an operon required for polyferation or that has an activity against a biological pathway or that has an activity against a biological pathway or the gene product or that has an activity against a biological pathway or equired for proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or on which the test compound that inhibits the compound activity and antibaction of an organism. The antibisense or collection of compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the contiferation of an organism. The antibense nucleic acids are useful for cellular proliferation of an organism. The antibense nucleic acids required for cellular proliferation of an organism. The strains for homologous nucleic acids required conting discovery processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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                                                                                                                                                                                                                                               Ohlsen KL,
Forsyth RA,
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45.0%; Pred. No. 7.4e-20;
iive 23; Mismatches 26
                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 77221; 1766pp; English.
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                                                                                                                                                                                                                                                    Malone C,
Carr GJ,
                                            21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00946993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00372851.
06-MAR-2002; 2002US-0362699P.
21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                     ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                              2003-029926/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                   WPI; 2003-029926
N-PSDB; ACA53167
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                                                                                                                                                                                                                                                         Wang L,
Wall D,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The A. Daumanni incoleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. Daumanni and other Acinecobacter species in a sample, in screening compounds for the ability to interfere with the A. Daumannii life cycle or to inhibit A. Daumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A. Daumannii protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to isolated Acinetobacter baumannii nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                            Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent.
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(first entry)

63 9

ABU16869 standard; protein; 109 AA

RESULT 14
ABU16869
ID ABU1

(first entry)

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the full and the statements given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proliferation of a cell. Also included are:

(1) a vector comprising a proliferation of a cell. Also included are:

(2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or the activity of a gene in an operior required for proliferation or the activity of a gene in an operior required for proliferation; (7) identifying a compound that influences the activity of identifying a gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (3) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required clantifying proteins or screening for homologous nucleic acids required for cludar proliferation are sectively. The activation of an organism or the solution of an organism or the sending acids required for cludar proliferation of an organism. The antisense nucleic acids required for cludar acids acids required for cludar acids 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                    Protein encoded by Prokaryotic essential gene #2396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 44793; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00372851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BLIT-) ELITRA PHARM INC.
                                                                                                                                                                                                            Acinetobacter baumannii
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                                                                                                                                                                                                                                                              WO200277183-A2.
                                                     19-JUN-2003
                                                                                                                                                                                                                                                                                                                   03-OCT-2002
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Wall D,
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for blants. The present sequence represents the amino acid sequence of an A.
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63
              2 INQVDFFKCLSDQTRINILKLVLNKQNICVCELTEQLELSQPKISRHLALLTHGVLLDE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LIPLOLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 6454; 328pp; English.
                                                                                                                                                                                                                                                            Acinetobacter baumannii protein #2328.
                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 KOGKWVHYRLSPHIPSWAAQIIE 86
                                                                                        84
                                                                                                                                                                   ADA35167 standard; protein; 116 AA.
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                                                                               62 RKGQWVYYSINPDLPVWALDILK
                                                          64 KQGKWVHYRLSPHIPSWAAQIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00328352
                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                        Acinetobacter baumannii
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                baumannii protein.
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Search completed: June 2, 2004, 19:36:54

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Gарв ., 0

Length 109;

Query Match 44.9%; Score 227; DB 6; Length 10 Best Local Similarity 49.4%; Pred. No. 9.4e-20; Matches 41; Conservative 18; Mismatches 24; Indels

Job time : 58 secs

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Sequence 11993, A Sequence 25372, A Sequence 25372, A Sequence 25172, A Sequence 6454, Ap Sequence 2984, Ap Sequence 7179, Ap Sequence 7179, Ap Sequence 7179, Ap Sequence 6033, Ap Sequence 7724, Ap Sequence 27596, Ap Sequence 27596, Applit Sequence 2
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Sequence 19163, A
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227.624 Million cell updates/sec
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506
1 MIQLTPLQLPKULSDETRLG......PSWAAQIIBQAWLSQQDDVQ
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-25372
US-09-328-352-8212
US-09-328-352-6454
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-09-198-452A-1135
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US-09-252-991A-19163
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US-09-489-039A-9929
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US-09-543-681A-4561
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US-09-134-000C-6033
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                                                                                                                                                                                                                                                                                                                                                389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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No.
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Sequence 8144, Ap Sequence 24784, A Sequence 69, Appl Sequence 87, Appl Sequence 1764, A Sequence 0550, Ap Sequence 2733, A Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 4473, Ap	estatenhistaan. 1	ACID SEQUENCES RELATING TO KLEBSIELLA TICS AND THERAPEUTICS	Length 112; Indels 0; Gaps 0;	MLOLTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCWALDOSOPKISRHLAMIRESGIL 60 ::	QUENCES RELATING TO PROTEUS MIRABIL
US-09-469-039A-8144 US-09-252-991A-24784 US-09-228-986-68 US-09-693-542-87 US-09-693-542-87 US-09-693-542-87 US-09-489-039A-9484 US-09-489-039A-9484 US-09-589-619-5 US-09-899-619-5 US-09-489-039A-9576 US-09-899-039A-9576 US-09-389-619-5 US-09-389-619-5 US-09-489-039A-9576 US-09-489-039A-9576 US-09-481-418-2 US-09-461-418-2 US-09-461-418-2 US-09-107-532A-4473 US-08-107-532A-4473 US-08-107-532A-4473	ALIGNMENTS	RESULT 1 US-09-489-039A-11993 ; Sequence 11993, Application US/09489039A ; Patent No. 6610836 ; GENERAL INFORMATION: APPLICANT: GATY BRECON Et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUEN ; TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THEI ; TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THEI ; CURRENT APPLICATION NUMBER: US/09/489,039A ; CURRENT FILING DATE: 1999-01-29 ; NUMBER OF SEQ ID NOS: 14342 ; SQ ID NO 11993 ; LENGTH: 112 ; TYPE: PRI ; TYPE: PRI ; CORGANISM: Klebsiella pneumoniae US-09-489-039A-11993	Score 432; DB 4; 1 Pred. No. 3e-49; 10; Mismatches 7;	MLOLTPLQLFKOLLSDETRLGIVLLIREMGELCVCDLCW ::	ULT 2 99-543-691A-7062 equence 7062, Application US/09543681A atent No. 6605709 EBREAL INFORMATION: TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709-1002-001 CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT APPLICATION NUMBER: US 60/128,706 PRIOR APPLICATION NUMBER: US 60/128,706 NUMBER OF SEQ ID NOS: 8344 TYPE: PRI TYPE
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		lication US reton et. a reton et. a . NUCLEIC . NUCLEIC . NUCHERC . NUCHERC . NUMBER: U E. 2000-01 E. 2000-01 E. 2000-12 OS: 14342 lla pneumon	85.4%; larity 82.5%; Conservative :	QLFKNLSDETR 	ULT 2 09-43-681A-7062 09-543-681A-7062 atent No. 6605709 AEDLICANT: GARY BRETON TITLE OF INVENTION: TITLE OF INVENTION: NUCLEIC ACID AND AM. TITLE OF INVENTION: DIGANOSTICS AND THE FILE REFERENCE: 2709.1002-001 CURRENT APPLICATION NUMBER: US/09/543,60 CURRENT FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344 LENGTH: 119 TYPE: PRT TYPE: PRT
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		A-11993 993, App 6610836 6610836 00RMATION NWENTION NWENTION EBNCE: 2 PPLICATION LILING DAT 1.1CHO	h Similarity 80; Conser		1A-7062 062, Appl 6605709 FORMATION INVENTION INVENTION INVENTION INTING DAI TICATION TILING DAI TICATION ING DAIR: SEQ ID N
229 229 230 331 331 332 333 334 335 337 337 338 337 338 338 338 338		LT 1 9-489-035 9-689-035 quence 11 tent No. meral INL ITLE OF 1 IT	Query Match Best Local S Matches 80	1 3 61 63	RESULT 2 US-09-541-681A-7062 Sequence 7062, Appli Patent No. 6605709 GENERAL INFORMATION: TITLE OF INVENTION: FILE REFERENCE: 270 CURRENT APPLICATION CURRENT APPLICATION PRIOR APPLICATION PRIOR PELING DATE: NUMBER OF SEQ ID NC SEQ ID NO 7062 ILENGTH: 119 TYPE: PRI
		RESULT US-09-09-09-09-09-09-09-09-09-09-09-09-09-	988	3 8 5 8	RESULT US-09-1 Sequel Patel RESULT TITI TITI TITI PRII PRII RESULT TITI TITI TITI TITI TITI TITI TITI T

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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252
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Sequence 6671, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
PILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
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COMPUTER READMBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
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                                                                                                      63 RKOGKWVHYRLSPHIPSWAAQIIE 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Acinetobacter baumannii
US-09-328-352-6454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
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Best Local Similarity 49.4%;
Matches 41; Conservative 1:
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                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.6%; Score 266; DB 4; Length 142; 51.6%; Pred. No. 3e-27;
                                                                          Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Indels
                                                                      Ouery Match 59.9%; Score 303; DB 4; Length 11 Best Local Similarity 63.4%; Pred. No. 3.2e-32; Matches 59; Conservative 13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 KQGKWVHYRLSPVLLPWVKNIIDITYTTEKNRV 101
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US-09-328-352-8212
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US-09-252-991A-25372
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Best Local Similarity 51.v.,
Best Local Scholarity 51.v.,
A8; Conservative
                    ORGANISM: Proteus mirabilis
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Best Local Similarity
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                              ; UKGANISM: FIUCEN
US-09-543-681A-7062
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US-09-328-352-8212
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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Sequence 7083, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette AID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BUTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                      FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
SEQ ID NO 2984
LENGTH: 110
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 117
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CORRESPONDENCE ADDRESS:
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Matches 24; Congery
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Matches 28; Conserv
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR PELING DATE: 1997-108-14
SEQ ID NOS: S674
SEQ ID NOS: S674
LENGTH: 127
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; Sequence 2984, Application US/09134001C
; Setent No. 6380370
; GENERAL NO. 6380370:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.2%; Score 127.5; DB 4; Length Best Local Similarity 38.2%; Pred. No. 3.5e-09; Matches 29; Conservative 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 24.9%; Score 126; DB 4;
1 Similarity 39.1%; Pred. No. 7.2e-09;
27; Conservative 15; Mismatches 25.
                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...105
SEQUENCE DESCRIPTION: SEQ ID NO: 6671:
                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2896, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis
          TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                           LENGTH: 105 amino acids TYPE: amino acid
                                             INFORMATION FOR SEQ ID NO: 6671:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WTHYSLSKSGSEYASK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 WVHYRLSPHIPSWAAQ 83
                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 GTWNYÝKIN 110
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                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  JS-09-107-532A-6671
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                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM:
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Matches
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GENERAL INFORMATION:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: UDGANOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENY APPLICATION NUMBER: US/09/543,681A
CURRENY FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mueller, Joachim
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REPERBURE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT PILING DATE: 1999-10-07
BARLIER APPLICATION NUMBER: DE 198 46 493.2
BARLIER PILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 LFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKW 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 LFXNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKW 68
                                                                                                                                                                                                  Gaps
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83.5; DB 4; Length 121;
Pred. No. 0.0026;
5; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09413814

Patent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
                                                                             Length 124;
                                                                           Query Match
16.8%; Score 85; DB 4; Le
Best Local Similarity 28.4%; Pred. No. 0.0017;
Matches 23; Conservative 21; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7179, Application US/09543681A
Patent No. 6605709
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4197
                                                                                                                                                                                                                                                                                                             : | : | : | : | : | : | 91 MIYSIDDIHVSTLLKQAIHHS 111
                                                                                                                                                                                                                                                                              69 VHYRLSP-HIPSWAAQIIEQA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Chopherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.8%;
Matches 21; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRGANISM: Proteus mirabilis US-09-543-681A-7179
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96 IFYSIA 101
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US-09-543-681A-7179
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Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PRILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
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               ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                             PAPPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...120
; SEQUENCE DESCRIPTION: SEQ ID NO: 7083:
US-09-107-532A-7083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 120 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 7083: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                           CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 KVVYYSLA 98
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US-09-134-001C-4197
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LENGTH: 124
TYPE: PRT
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Search completed: June 2, 2004, 19:39:23 Job time : 23 secs
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; APPLICANT: Marc J. Rubenfield et al.
; APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: NUCLEIC ACID AND AMINOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19998
; LENGTH: 348
; TYPE: PRT
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LSDETRLGIVLLIREMGELC----VCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKW 68
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                                                                                                                                                                                                                                                                                          5; Gaps
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16.1%; Score 81.5; DB 4; Length 120;
Best Local Similarity 33.3%; Pred. No. 0.0048;
Matches 22; Conservative 14; Mismatches 25; Indels
                                                                                                                                                            Query Match
16.3%; Score 82.5; DB 3; Length 118;
Best Local Similarity 36.1%; Pred. No. 0.0035;
Matches 22; Conservative 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6033, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                          ); ORGANISM: Sorangium cellulosum US-09-413-814-17
SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 VHYRLS 74
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                                                  118
                                                                      TYPE: PRT
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9 LFKNLSDETRIGIVILLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKW 68
                                                                                                                                            Gaps
                                                                                      1;
                                                 Length 348;
                                                                                    Indels
                                                                                      48;
                                              Query Match
Best Local Similarity 25.3%; Pred. No. 0.12;
Matches 22; Conservative 16; Mismatches 48;
                                                                                                                                                                                                                                      93 IFYRRSLPLAERTGGALHAALLEEVDE 119
                                                                                                                                                                                                    69 VHYRLSPHIPSWAAQIIEQAWLSQQDD 95
, ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19898
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55916, A
55373, A
681651, A
66368, A
77221, A
44793, A
62327, A
643327, A
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Sequence 59876, A
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                                                                                                                                                                                                           June 2, 2004, 19:38:22; Search time 43 Seconds (without alignments) 634.648 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: \cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
3: \cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB_pep:*
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6: \cgn2_6/ptodata/2/pubpaa/US07_NBW_PUB_pep:*
7: \cgn2_6/ptodata/2/pubpaa/US08_NBW_PUB_pep:*
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9: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_pep:*
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11: \cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB_pep:*
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19: \cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_pep:*
19: \cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB_pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-282-122A-43386
US-10-282-122A-55916
US-10-282-122A-55916
US-10-282-122A-65913
US-10-282-122A-69031
US-10-282-122A-68165
US-10-282-122A-6316
US-10-282-122A-6316
US-10-282-122A-77221
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US-10-282-122A-62327
US-10-282-122A-64752
US-10-156-761-7873
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Maximum Match 100%
Listing first 45 summaries
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1 MLQLIPEQLFKNLSDETRLG...
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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Perfect score:
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ALIGNMENTS

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1 MLQLTPLQLFRNLSDETRLGIVLLLRENGELCVCDLCMALDQSQPKISRHLAMLRESGIL 60
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                                                                                                   APPLICANT: Regenesis
APPLICANT: Regenesis
APPLICANT: Laing, Lance
AITLE DE INVENTION: BIOSENSOR FOR SMALL MOLECULE ANALYTES
FILE REFERENCE: 4107/11.443-US.
CURRENT APPLICATION NUMBER: US/10/222,952A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,714
PRIOR APPLICATION NUMBER: US 60/313,714
STOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 506; DB 14; Best Local Similarity 100.0%; Pred. No. 2.4e-54; Matches 97; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
DATABARS ACCESSION NUMBER: GenBank / CAA 34168
DATABARSE ENTRY DATE: 1994-09-07
RELEVANT RESIDUES: (1)..(117)
                   Sequence 2, Application US/10222952A Publication No. US20030096275A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-222-952A-2
US-10-222-952A-2
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERBNCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-010-23
PRIOR PILING DATE: 2000-01-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed - See File Wrapper or FALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 80.9%;
Matches 76; Conservative I:
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Zyskind, Judith
Wall, Daniel
                                                                                            Robert
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Wall, Daniel
Trawick, John
Carr, Grant
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US-10-282-122A-43386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITAA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%; Pred. No. 4e-45; Length 109;
Matches 80; Conservative 9; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-19-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-16
PRIOR FILING DATE: 2001-02-09
                   -10-282-122A-59876
Sequence 59876, Application US/10282122A
Publication No. US20040029129A1
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                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Forsyth, R.
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US-10-282-122A-43386
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Gaps

Length 117;

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4 LIPIQLFKILADETRIGIVLLLSELGELGVCDLCTALDQSQFKISRHLALLRESGLLLDR
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4 LIPLOLFKNISDETRIGIVILLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
                                                                                                  64 KQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
                                                                                                                              FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                 Sequence 77709, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Carr, Grant
Yamamoto, Robert
ForByth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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FILING DATE: 2000-09-09
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Best Local Similarity
Matches 60; Conserv
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US-10-282-122A-55373
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LENGTH: 106
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 77709
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.9%; Score 399; DB 12; Length 113; 76.0%; Pred. No. 3.7e-41; tive 13; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LDRKOGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDV 96
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                         PRIOR APPLICATION NUMBER: 60/191, 079
PRIOR PILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-10-23
PRIOR PILLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-12-22
PRIOR PILLING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-20
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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ORGANISM: Yersinia pestis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 73; Conserv
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APPLICANT:
APPLICANT:
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## PRIOR APPLICATION NUMBER: 60/42,798

## PRIOR APPLICATION NUMBER: 60/42,478

## PRIOR APPLICATION NUMBER: 60/425,425

## PRIOR PRING DATE: 2000-10-23

## PRIOR PRILICATION NUMBER: 60/220:347

## PRIOR PRILICATION NUMBER: 60/220:343

## PRIOR PRILICATION NUMBER: 60/22
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; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-10-282-122A-69031
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APPLICANT:
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PRIOR PADLICATION NUMBER: 60/194,078

PRIOR PADLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-19-09

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-22

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
          PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55373
LENGTH: 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.6%; Score 327; DB 12; 70.4%; Pred. No. 2.7e-32; tive 14; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 69031, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Enterobacter cloacae FEATURE: NAME/KEY: MISC_FEATURE: LOCATION: (63)...(63)...(53)...(53)...(51)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(53)...(5
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APPLICANT: Asmudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Yeskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
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Best Local Similarity
Matches 57; Conserva
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US-10-282-122A-69031
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of EBSential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2008-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-12-22
PRIOR PRILING DATE: 2001-02-09
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                                                                                                                                      4 LTPLOLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
                                                                      Gaps
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   Length 111;
                                                                   Indels
Query Match
59.9%; Score 303; DB 12;
Best Local Similarity 63.4%; Pred. No. 2.5e-29;
Matches 59; Conservative 13; Mismatches 21;
                                                                                                                                                                                                                                                                               64 KOGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDV 96
                                                                                                                                                                                                                                                                                                                                61 KQGKWVHYRLSPVLLPWVKSIIDITYTTEKNRV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 68165, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Mall, Daniel
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-68165
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US20040029129A1
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APPLICANT:
APPLICANT:
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   2 ITPPDVFKSLSDETRARATLLIASLGELCVCELMCALNDSQPKISRHLAQLRSNGMLLDR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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                                                               64 KOGKWVHYRLSPHIPSWAAQIIE-----QAWLS 91
                                                                                                                          62 RÓGOWYYYRLNPELPSWVHEMLQVTLQANSQWLA 95
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-0.20

PRIOR FILING DATE: 2000-0.3-21

PRIOR PAPLICATION NUMBER: 60/206, 848

PRIOR PAPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/203,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-09

PRIOR PELING DATE: 2000-09-09

PRIOR PELING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR PELING DATE: 2001-12-22

PRIOR PELING DATE: 2001-12-22

PRIOR PELING DATE: 2001-12-22

PRIOR PELING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                      Sequence 66368, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cherlos
APPLICANT: Malone, Cherlot
APPLICANT: Alone, Cherlot
APPLICANT: Alone, Cherlot
APPLICANT: Ohleen, Kari
APPLICANT: Ohleen, Kari
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Travick, Grant
APPLICANT: Travick, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yersyth, R.
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US-10-282-122A-77221
; Sequence 77221, Application US/10282122A
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 48; Conserva
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LENGTH: 116
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4 LIPLOLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR 63
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RQGQWVFYRISDQLPGWMRKQIQGLVESNCLKQEYQQDIQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 KOGKWVHYRLSPHIPSWAAQ----IIEQAWLSQ--QDDVQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.1%; Score 228; DB 12;
45.0%; Pred. No. 4.5e-20;
live 23; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-05-06
PRIOR PAPLICATION NUMBER: 60/230,335
PRIOR PELLING DATE: 2000-09-06
PRIOR PELLING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR PELLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin version 3.1 SEQ ID NO 77221
                                                                                                                    Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoco, Robert
Forsyth, R.
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-282-122A-44793
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APPLICANT:
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Gaps

5

Indels

Length 134;

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8 QLFXNLSDETRIGIVLLL--REMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQ 65
                                                                                                                                                                                                                       Query Match
31.6%; Score 160; DB 14;
Best Local Similarity 41.2%; Pred. No. 1.4e-11;
Matches 33; Conservative 17; Mismatches 28;
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 7001-02-16
PRIOR FILING DATE: 7001-02-16
PRIOR FILING DATE: 7001-02-16
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CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11291
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: GHERA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTOORI, MASAHIKA
TITIE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200, 335
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR APPLICATION NUMBER: 60/243, 625
PRIOR PILING DATE: 2000-110-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11291, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|:||:| |:| |:| |::
62 RKGQWVYYSLNPDLPVWALDILK 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin version 3.1
SEQ ID NO 44793
LENGTH: 109
  Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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Best Local Similarity
Matches 41; Conserv
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US-10-156-761-11291
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILLS OF INVENTION: Identification of Essential Genes in Microorganisms
FILLS OF INVENTION NUMBER: 05/102/22.122A
CURRENT PILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-07
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
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29.8%; Score 151; DB 12;
Best Local Similarity 42.6%; Pred. No. 1.6e-10;
Matches 29; Conservative 15; Mismatches 22;
                                                                                                                                                                                                                                        Sequence 62327, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                   97 GTWVYYWLVPEMTDRLASIL 116
66 GKWVHYRLSPHIPSWAAQII 85
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Fawick, John
APPLICANT: Foreyth, R.
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SEQ ID NO 62327
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35 FKALADPVRLQLLSSVASRAGGEACVCDISAGVEVSQPTISHHLKVLRDAGLLTSRRRAS 94

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/202,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-22
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 64752
LENGTH: 126
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                                                                                                                       RESULT 14
US-10-282-122A-64752
US-10-282-122A-64752, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR PEDICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PEDING DATE: 2000-10-03
PRIOR PEDICATION NUMBER: 60/242, 578
PRIOR PEDICATION NUMBER: 60/243, 625
PRIOR PAPLICATION NUMBER: 60/253, 625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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US-10-156-761-7873
; Sequence 7873, Application US/10156761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64752
                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                        Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                               WVYYAVVP 102
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68 WVHYRLSP 75
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Best Local Similarity
Matches 29; Conserva
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| PUBLICATION NO. US20030119018A1
| GENERAL INFORMATION:
| APPLICANT: OWGRA, SATOSHI
| APPLICANT: INEXDA, HARUO
| APPLICANT: ISHIRAWA, JUN
| APPLICANT: SHIBA, TADAYOSHI
| APPLICANT: SALAKI, WOSHITUKI
| TILE OF INVERTION: NOVEL POLYNUCLECTIDES
| FILE REFERENCE: 1249-262
| CURRENT FILING DATE: 2001-05-30
| PRIOR FILING DATE: 2001-05-30
| PRIOR FILING DATE: 2001-06-50
| PRIOR PILING DATE: 2001-06-02
| PRIOR PILING DATE: 2001-06-02
| PRIOR PILING DATE: 2001-06-02
| PRIOR FILING DATE: 2001-06-02
| PRIOR PILING DATE: 2001-06-02
| PRIOR PILING DATE: 2001-06-02
| PRIOR FILING DATE: 2001-06-02
| PRIOR PILING DATE: 2001-06-02
| PRIOR PRIDE SEQUENCE: PRIOR PRIOR DATE: 1009
| PRIOR PILING DATE: 2001-06-02
| PRIOR PRIOR PRIOR DATE: 2001-06-02
| PRIOR PRIOR PRIOR DATE: 2001-06-02
| PRIOR PRIOR PRIOR DATE: 2001-06-02
| PRIOR PRIOR DATE: 2001-06-03
| PRIOR PRIOR DATE: 2001-06-02
| PRIOR PRIOR DATE: 2001-06-02
| PRIOR PRIOR DATE: 2001-06-03
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model using sw search, protein OM protein

2, 2004, 19:34:56; Search time 21 Seconds (without alignments) 444.313 Million cell updates/sec June Run on:

US-10-676-296-2_COPY_1_97 506 1 MLQLTPLQLFKNLSDETRLG... Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

.....PSWAAQIIEQAWLSQQDDVQ

283366 283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

transcription regu transcription regu transcription regu transcription regu arsenical resistan hypothetical prote hypothetical prote arsenical resistan Arsk protein PA227 transcription regu transcription regu arsenical resistan hypothetical prote hypothetical prote transcription regu hypothetical prote ypothetical prote arsenical resistan transcription regu transcription regu probable transcrip transcription regu heavy metal regist cadmium efflux sys transcription regu cadmium-binding pr transcription regu Description SUMMARIES E91175 A56269 AD0406 F83361 G82245 B69220 G70420 AG2151 S74901 H84024 AD1944 F70964 H72306 AF1212 Query Match Length DB 131 130.5 130.5 129 127 124.5 423 423 414 399 266 228 181 176 156.5 156.5 151 151 151 151 151 151 147 142 137.5 136.5 Score Result

probable transcrip	transcription repr	probable transcrip	probable transcrip	transcription regu	probable transcrip	transcription repr	, hypothetical prote	smtB protein - Syn	hypothetical prote	arsenical resistan	arsenical resistan	hypothetical prote	probable ArsR-fami	transcription regu	transcription regu
D97176	D75141	E70585	F95983	G69106	C95333	A75601	A82658	831197	C75193	B41903	A41902	F89962	C87012	AI2982	F98300
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	23.8	23.8		23.5	23.4	23.3	22.4	22.2		22.0	21.8	21.8	21.8	21.5	

ALIGNMENTS

RESULT 1	
BVECAR	
arsenical	arsenical resistance operon repressor - Escherichia coli plasmid R773
C;Species	C; Species: Escherichia coli
C;Date: 3	C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accessi	C; Accession: JS0448
R;San Fra	R; San Francisco, M.J.D.; Hope, C.L.; Owolabi, J.B.; Tisa, L.S.; Rosen, B.P.
Nucleic A	cids Res. 18, 619-624, 1990
A;Title:	A; Title: Identification of the metalloregulatory element of the plasmid-encoded arsenica
A;Referen	A; Reference number: JS0448; MUID: 90174986; PMID: 2408017
A; Accessi	A; Accession: USO448
A; Molecul	A; Molecule type: DNA
A:Residue	A;Residues: 1-117 <san></san>
A; Cross-r	
C;Comment	C, Comment: This is a transcriptional repressor for the ars operon; it is a trans-acting
C;Genetics:	
A; Gene: arsR	ISB
A.Genome: plasmid	plasmid
C;Superfa	C; Superfamily: arsenical resistance operon repressor
C; Keyword	C. Keywords: DNA binding; homodimer; repressor; transcription regulation
Query Match	100.0%;
Best Lo	0%; Pred. No. 1.6e-50;
Matches	97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
à	1 MLOLTPLOLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGIL 60
qo	1 MIQLTPLQLFKNLSDETRLGIVLLIREMGELCVCDLCMALDQSQPKISRHLAMLRESGIL 60
λō	61 LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
đa	61 LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97

C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Mature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Accession: E86021
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-117 <STO>
A;Residues: 1-117 <STO>
A;Cross-references: GB:AE005174; NID:g12518198; PIDN:AAG58633.1; GSPDB:GN00145; UWGP:Z49
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics: hypothetical protein arsR [imported] - Escherichia coli (strain O157:H7, substrain EDL93

transcription regu arsenical resistan

Query Match

Best Loca Matches

RESULT 3

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R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Refession: H65147
A;Recession: H65147
A;Restius: preliminary; nucleic acid sequence not shown; translation not shown A;Rolcoule type: DNA
A;Residues: 1-117 < BLAT>
A;Cross-references: GB:AE000426; GB:U00096; NID:g1789910; PIDN:AAC76526.1; PID:g1789916; A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arsk protein PA2277 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
S;Stover, C.K.; Pham, X.Q.; Erwin, A.I.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br R;Stover, C.K.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arsenical resistance operon repressor [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AD0406
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Attle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Residues: 1-113 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92576.1; PID:g15981273; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 414; DB 2; Length 11
Pred. No. 5.3e-40;
...---+ches 7; Indels
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78.9%; Score 399; DB 2;
Best Local Similarity 76.0%; Pred. No. 2.6e-38;
Matches 73; Conservative 13; Mismatches 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 77.5 min
C;Superfamily: arsenical resistance operon repressor
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ilarity 80.9%;
Conservative 1:
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ses 76; Conserv
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C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Jate: 03-0ct-1995 #sequence revision 03-0ct-1995 #text_change 01-Mar-2002
C;Accession: A55269; 847721; #65147
R;Diorio, C.; Cai, J.; Marmor, J.; Shinder, R.; DuBow, M.S.
B;Diorio, C.; Cai, J.; Marmor, J.; Shinder, R.; DuBow, M.S.
A;Title: An Escherichia coli chromosomal ars operon homolog is functional in arsenic det
A;Reference number: A56269; MUID:95238276; PMID:7721697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: E9175
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gencha; Pritle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gencha; Pratus: preliminary
A; Accession: E91175
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-117 <HAY>
A; Residues: 1-117 <HAY>
A; Residues: 1-117 <HAY>
A; Cross-references: GB: BA000007; PIDN: BAB37796.1; PID: g13363847; GSPDB: GN00154
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: arsenical resistance operon repressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein EC64373 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
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A;Molecule type: DNA
A;Residues: 1-117 <PLU>
A;Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18477.1; PID:g466638
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                                                                                                                          Length 117;
                                                                                                                                                                                        Indels
                                                                                                                       Match 83.6%; Score 423; DB 2; L Local Similarity 84.0%; Pred. No. 4.9e-41; les 79; Conservative 8; Mismatches 7;
                                  A;Gene: arsR
C;Superfamily: arsenical resistance operon repressor
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Local Similarity ses 79; Conserv

Best Loc Matches

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à d RESULT 4

Query Match

Status: preliminary Molecule type: DNA Residues: 1-117 <DIO>

3 10:25:25 2004

Thu Jun

Best Loca Matches

RESULT G82245

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A,Cross-references: GB:AE000865, GB:AE000666; NID:g2621984, PIDN:AAB85397.1, PID:g262199
A,Experimental source: strain Delta H
C,Genetics:
C,Genetics:
C,Superfamily: arsenical resistance operon repressor
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000737; NID:g2983782; PIDN:AAC07355.1; PID:g2983797; GB:AE00065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: G70420
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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A;Cross-references: GB:BA000019; PIDN:BAB74465.1; PID:g17131859; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 26-Aug-1999
C;Accession: G70420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 QLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S RIFYALSEPKRICMVKLILEREBLCVCDFMRIFKESQPKISFHLKVLREAGLVTSQKRGK
                                                                                                                                                                                                                                                                                                                                         11 KNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKWVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                                            Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transcription regulator ArsR family - Aquifex aeolicus
                                                                                                                                                                                                                      35.8%; Score 181; DB 2;
51.9%; Pred. No. 2.2e-13;
tive 11; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: arsenical resistance operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | :|| | :||
102 YSLASDDLPSMIKQVIE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 YRL-SPHIPSWAAQIIE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Experimental source: strain VF5
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Best Local Similarity 49.38
...-rhes 35; Conservative
                                                                                                                                                                                                                            Query Match 35.8% Best Local Similarity 51.9% Matches 40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WNYYRLNKEAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 1-102 <AQF>
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A,Gene: are
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C;Accession: B69220
E;Santh, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J-Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A,Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: F83361
                                                                                                                                       A;Residues: 1-116 <STO>
A;Cross-references: GB:AE004653; GB:AE004091; NID:g9948298; PIDN:AAG05665.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: GB:AE004188; GB:AE003852; NID:99655530; PIDN:AAF94227.1; GSPDB:GN001
A,Experimental source: serogroup O1; strain N16961; biotype Bl Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82245
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C,Species: Methanobacterium thermoautotrophicum
C,Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                              TPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SPAEVFKCLADETRVRATILIVDQGELCVCELMCALADSQPKISRHLAQLRSAGLILDRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LIPLOLFKNISDETRIGIVILLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                         23; Indels
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51.6%; Pred. No. 4.1e-23;
tive 22; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | : | | : | : | : | : | : | : | : | CGOWUYYRLNPALPAWIHEVLQVTLRANGDWLQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
                                                                                                                                                                                                                                                                                                                                                                         Conservative
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les 45; Conserv
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-113 <HEI>
                                                                                        A;Status: preliminary A;Molecule type: DNA
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A;Gene: arsR; PA2277
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A;Gene: VC1068
A;Map position: 1
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A; Experimental source: strain H37Rv

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> RESULT 11 S74901

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transcription regulator, ArBR family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87514
E;Accession: D87514
E; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
E; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T36631
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999
A;Reference number: Z21610
A;Accession: T36631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AL078610; PIDN: CAB44399.1; GSPDB:GN00070; SCOEDB: SCH35.28cA; Experimental source: strain A3(2)
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A;Gene: CC2141
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                                                                                                                                                                                                                                                                                              probable transcription regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 QLFKNLSDETRIGIV--LLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQ
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                                                                                                                                       Length 126;
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                                                                                                                                       Query Match 29.8%; Score 151; DB 2; 1
Best Local Similarity 42.6%; Pred. No. 6.2e-10;
Matches 29; Conservative 15; Mismatches 22;
                       C;Genetics:
A;Gene: Rv2542
C;Superfamily: arsenical resistance operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: SCOEDB:SCH35.28c
C;Superfamily; arsenical resistance operon repressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 WYYAVVP 102
                                                                                                                                                                                                                                                                                                                                                                                                 68 WVHYRLSP 75
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Best Local Similarity
Matches 33; Conserv
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Matches 30; Conserv
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A; Status: preliminary
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A,Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A,Authors: Capres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A,Atfiele: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A,Reference number: A70500; MuID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: GB: Z80225; GB: AL123456; NID: 93242265; PIDN: CAB02348.1; PID: 91550683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BAA17862.1; PID:g165294
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                 16 FHALSDPIRINVLELLRQR-ELCVCDLCEALGVSQSKLSFHLKTLKEASLVNSRQQGRWI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arsenical resistance operon repressor - Synechocystis sp. (strain PCC 6803) N,Alternate names: protein s111957 C;Species: Synechocystis sp. C;Species: Synechocystis sp. C;A.Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: S74901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Rv2642 - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 FKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKWV
                                                                                                                                                                                                                                             10 FKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 104;
                                                                                                                         Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Accession: 874901
A, Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                  Indels
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                                                                                                                   Query Match 32.9%; Score 166.5; DB 2; Best Local Similarity 47.2%; Pred. No. 9.8e-12; Matches 34; Conservative 16; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obs.; Score 156.5; DB 2; Local Similarity 48.5%; Pred. No. 1.2e-10; Local 32; Conservative 14; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: arsA
A,Start codon: GTG
C,Superfamily: arsenical resistance operon repressor
C;Genetics:
A;Gene: alr2766
C;Superfamily: arsenical resistance operon repressor
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Molecule type: DNA Residues: 1-104 <KAN>

Genetics:

HYRLSP 75 YYRLNP 77

10 72

ð a ð Molecule type: DNA; Residues: 1-126 <COL>

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7 LOLFKOLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQG 66
                                 SERVIRAAGESTRIRILALL-AAEELSVJELCRILDQSQPRVSRHIKILAEAGLVERFPDG 67
                                                        셤
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67 KWVHYRLSPHIPSWAAQIIEQA 88

à

68 AWVFYRLAAKSP--GRLLUVEQA 87

hypothetical protein MJ1325 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Accession: D64465
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Fleich, C.J.; Wortbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Felch, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64465
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-89 <BULL>

A;Cross-references: GB:U67573; GB:L77117; NID:g2826395; PIDN:AAB99335.1; PID:g1592329; C;Genetics:

A;Map position: FOR1275430-1275699 C;Superfamily: arsenical resistance operon repressor

ö Query Match
29.1%; Score 147; DB 2; Length 89;
Best Local Similarity 45.3%; Pred. No. 1.2e-09;
Matches 29; Conservative 12; Mismatches 23; Indels

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Gaрв

8 QLFYNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGK 67

ŏ g ý qq

SELEKAFGDPTRLMILKLLAENGSMCVCKIIDELKKPQPTISHHLNILKKAGIVKARKEGT 68

68 WVHY 71

WNFY 72

2, 2004, 19:38:48

Search completed: June Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 2, 2004, 19:31:11; Search time 17 Seconds (without alignments) 297.106 Million cell updates/sec

Title: Perfect score:

US-10-676-296-2_COPY_1_97
506
1 MIQLTPLQLFKNLSDETRLG......PSWAAQIIBQAWLSQQDDVQ 97 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	P15905 escherichia P52144 escherichia P52144 escherichia P37374 staphylococ Q58721 methanococc Q58721 methanococc Q58721 methanococc Q58724 bacillus su P45949 bacillus su P45949 bacillus su P45949 bacillus su P30338 staphylococ P52659 vibrio chol P20007 staphylococ P52659 vibrio chol P20007 staphylococ P52659 vibrio chol P20007 staphylococ Q58948 methanococc Q58948 methanococc Q58948 methanococc Q68323 methanococc Q88333 methanococc Q88313 methanococc Q88313 methanococc Q88313 methanococc Q88311 methanococc Q88311 methanococc Q89388 homo sapien Q59988 homo sapien Q59988 homo sapien Q13367 homo sapien Q59988 homo sapien
SU	ARRI ECOLI ARRZ ECOLI ARRZ ECOLI CADE STRAU YD25 METUJA CADE LISNO CADE LISNO CADE LISNO CADE SYND7 ARSR STRAY ARSR STRAI ARSR STRAI ARSR STRAI ARSR STRAI ARSR STRAI ARST STRAI YF53 METUJA ARTH LEIDO XY74 METUJA ARTH RALSO YR72 ARATH BAGT BACAN IMDH TRYBB PROCA MODE STRAY ARTH RALSO YR72 ARATH ARTH RALSO YR72 ARATH ARTH RALSO YR73 METUJA ARTH RALSO YR74 METUJA ARTH RALSO YR77 METUJA
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Length	1117 1117 1119 1119 1119 1119 1119 1119
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P24008 rattus norv P56114 helicobacte	Q10283 schizosacch P25243 bacteriopha O8tvm5 methanopyru	P33400 saccharomyc Q08493 homo sapien	P14376 escherichia P97793 mus musculu	Q10187 schizosacch P33233 escherichia	Q7vn67 haemophilus
S5A1_RAT GATA_HELPY	HMDH SCHPO VGA BPAL3 SYFA METKA	R101_YEAST CN4C_HUMAN	RCSC_ECOLI ALK MOUSE	YAWD SCHPO	FPG_HAEDU
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259	1053 494 524	625	949 1621	612 258	274
12.3	122.3	12.2	12.2	12.1	12.0
62	62 61.5 61.5	61.5	61.5 61.5	61	60.5
34	36 37 88	36,6	41	4.4 4.3	45

ALIGNMENTS

RESU ARR1	RESULT 1 ARR1 ECOLI	
요.	ARRI ECOLI STANDARD; PR	PRT; 117 AA.
) E	71.3005; 01.300.1990 (00) 14 (rested)	
ä	(Rel. 14, Last	sequence update)
DŢ	01-OCT-1996 (Rel. 34, Last annot	annotation update)
DE	esistance operon	essor.
S	ARSR.	
SO	Escherichia coli.	
8	Plasmid R773.	
ပ္ပ	Bacteria; Proteobacteria; Gammap	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
ပ္ပ	Enterobacteriaceae, Escherichia.	
XO	NCBI_TaxID=562;	
RN	_ [1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=90174986; PubMed=2408017;	
RA	San Francisco M.J.D., Hope C.L., Owolabi	Owolabi J.B., Tisa L.S., Rosen B.P.;
RT	"Identification of the metalloregulatory element of	gulatory element of the
RT	plasmid-encoded arsenical resistance operon.";	ance operon.";
RL	Nucleic Acids Res. 18:619-624(1990).	. (06
RN	[2]	
RP	FUNCTION.	
RX	MEDLINE=92157859; PubMed=1838573;	
RA	Wu J., Rosen B.P.;	
RŢ	"The ArsR protein is a trans-acting	ing regulatory protein.";
RL	Mol. Microbiol. 5:1331-1336(1991).	
RN	[3]	
RP	METAL-REGULATION.	
ΣX	MEDLINE=93107054; PubMed=8416957;	•
RA	Wu J., Rosen B.P.;	
RI	ų	the ars operon.";
RL	J. Biol. Chem. 268:52-58(1993).	
ပ္ပ	-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR FOR THE ARS OPERON.	PRESSOR FOR THE ARS OPERON. ARSR IS
ပ္ပ	A TRANS-ACTING REGULATORY PR	
ပ္ပ	EXPRESSION. THE REPRESSIVE E	
ပ္ပ	OF +III OXIDATION STATE OF A	OF +III OXIDATION STATE OF ARSENIC, ANTIMONY, AND BISMUTH, AS WELL
ប្ជ	AS ARSENATE (AS(V)).	
ပ္ပ	-!- SUBUNIT: Binds DNA as a homodimer.	dimer.

SUDDAL: DITCH DAY AS A DOMOGIMEY.
SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.

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PIR, JS0448; BVECAR.
HSSP; P30340; 1SMT.
InterPro; IRPO01845; HTH ArsR.
Pfam; PF01022; HTH 5; 1.
PRINTS; PR00778; HTHARSR. EMBL; X16045; CAA34168.1; -.

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                                                                                                                                                                                                                                       1 MLQLTPLQLFKNLSDETRIGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bruhn D.F., Li J., Silver S., Roberto F., Rosen B.P.;
Bruhn D.F., Li J., Silver S., Roberto F., Rosen B.P.;
Bruhn D.F., Li J., Silver S., Roberto F., Rosen B.P.;
Bruhn D.F., Li J., Silver S., Roberto F., Rosen B.P.;
FEMS Microbiol. Lett. 139-149-153 (1996).
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR FOR THE ARS OPERON. ARSR IS
A TRANS-ACTING REGULATORY PROTEIN WHICH CONTROLS ITS OWN
EXPRESSION: THE REPRESSIVE BFFECT OF ARSR IS ALLEVIATED BY OXYIONS
OF +111 OXIDATION STATE OF ARSENIC, ANTIMONY, AND BISMUTH, AS WELL
                                                                                                                                                                                                    1 MLQLTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCWALDQSQPKISRHLAMLRESGIL
                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00846; HTH ARSR_FAMILY; 1.
Plasmid; Arsenical resistance; Transcription regulation; Repressor; DNA-binding.
SMART; SM00418; HTH ARSR; 1.
PROSITE; PS00846; HTH ARSR FAMILY; 1.
Plasmid; Arsenical resistance; Transcription regulation; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AS ARSENATE (AS(V)).
-!- SUBUNIT: Binds DNA as a homodimer.
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                             100.0%; Score 506; DB 1; Length 117; 100.0%; Pred. No. 2e-48; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.3%; Score 447; DB 1; Length 117; 87.6%; Pred. No. 5.7e-42; ive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 H-T-H MOTIF (POTENTIAL).
12999 MW; 4E2D132F1F011AF6 CRC64;
                                                                      52 H-T-H MOTIF (POTENTIAL).
13198 MW; 1F0D10766E4FD886 CRC64;
                                                                                                                                                                                                                                                                                61 LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
                                                                                                                                                                                                                                                                                                            61 LDRKÇÇKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arsenical resistance operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001845; HTH ArsR.
Pfam; PF01022; HTH 5; 1.
PRINTS; PR00778; HTHARSR.
SMART; SM0418; HTH ARSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U38947; AAB09624.1;
                                                                                                                                                                    97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                            33
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P30340; 1SMT.
                                                                                                                                 Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid IncN R46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGULATORS.
                                                      DNA-binding.
DNA BIND
SEQUENCE 11
                                                                                                                                                                                                                                                                                                                                                                                                                  ARR2 ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
ARR2_ECOLI
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MEDLIRE=95298276; PubMed=7721697;

Diorio C., Cai J., Marmor J., Shinder R., Dubow M.S.;

Diorio C., Cai J., Marmor J., Shinder R., Dubow M.S.;

Man Escherichia coli chromosomal ars operon homolog is functional in arsenic detoxification and is conserved in Gram-negative bacteria.";

J. Bacteriol. 177:2050-2056 (1995).

-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR FOR THE ARSEFG OPERON. ARSE IS A TRANS-ACTING REGULATORY PROTEIN WHICH CONTROLS ITS OWN EXPRESSION. THE REPRESSIVE BFFECT OF ARSE IS ALLEVIATED BY OXYIONS OF +III OXIDATION STATE OF ARSENIC, ANTIMONY, AND BISMUTH, AS WELL AS ARSENTATE (AS VI) (BY SIMILARITY; BILANITY: BILANSCRIPTIONAL.

-!- SUBUNIT: Binds DNA as a homodimer (By similarity).

-!- SINILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                             STEATMERIZ / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
MLQLTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00046; HTH ARSR FAMILY; 1.
Arsenical resistance; Transcription regulation; Repressor;
DNA-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 H-T-H MOTIF (POTENTIAL).
13252 MW; 35BC3F6F94BBD3DB CRC64;
                                                                                                                                                                           61 LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.8%; Score 414; DB 1;
80.9%; Pred. No. 2.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                    117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arsenical resistance operon repressor. ARSR OR ARSE OR B3501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00418; HTH_ARSR; 1.
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PRINTS; PR00778; HTHARSR.
                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                           ECOLI
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                                                                                                                                                                                                                                                                                                                                                                        ARSR ECC
P37309;
                                                                                                                                                                                                                                                                                                                                            ARSR_ECOLI
ID ARSR ]
                                                                                                                                                                                                                                                                                                         RESULT 3
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Best Local Similarity

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Gaps

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87.6%;

Local Similarity 87.6 nes 85; Conservative

Best Loca. Matches

RESULT CADF ST

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last amontation update)
Cadmium efflux system accessory protein (Cadmium resistance regulatory
                                                                                                                                                                                                                                                                  MEDLINE=5637999; PubMed=8688087;
MEDLINE=9637999; PubMed=8688087;
MEDLINE=9637999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts R.M., Hilley Wasse C.R., Venter J.C.;
Klenk H.-P., Fraser C.M., Shith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 QLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MJ1325; -.
InterPro; IPR001845; HTH_ArsR.
Pfam; PF01022; HTH 5; 1.
SPRINTS; SM00418; HTHARSR; 1.
SMART; SM00418; HTH_ARSR; 1.
PROSITE; PS00846; HTH_ARSR_FAMILY; FALSE_NEG.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                            Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanoccales;
Methanocaldococcaceae; Methanocaldococcus.
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15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.1%; Score 147; DB 1; 45.3%; Pred. No. 2.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U67573; AAB99335.1; -.
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hes 29; Conserv
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SEQUENCE 89 AA;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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[1]
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      SOUR NEW WEEK STREET ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cadmium resistance determinants, and genes resembling the transposases genes of Thist.";
Submitted (FEB-193) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                               4 LIPIQLFKILADETRLGIVLLLSELGELCVCDLCTALDQSQPKISRHLALLRESGLLLDR
                                                                   4 LTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
      Gaps
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Chikramane S.G., Dubin D.T.;
"Pg1TD554: a Staphylococcus aureus chromosomal element encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription regulation; DNA-binding; Cadmium resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.3%; Score 163.5; DB 1; Length 40.9%; Pred. No. 5.5e-11; ive 19; Mismatches 28; Indels
      7; Indels
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cadmium efflux system accessory protein homolog.
                                                                                                                                                                                                                         89 AA
                                                                                                                                                                                      64 KQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ
                                                                                                                                                                                                                                                                                                                                                                                                        121 AA
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(Rel. 43, Last sequence update)
      11; Mismatches
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SMART; SM00418; HTH ARSR; 1.
PROSITE; PS00846; HTH ARSR FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001845; HTH_ArBR.
Pfam; PF01022; HTH 5; 1.
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Best Local Similarity 40.9°
      76; Conservative
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YD25_METJA
ID YD25_METJA
AC QS87Z1;
DT 15-MAR-2004 (
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Gaps ..

Length 89; 23; Indels 67

119 AA.

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REGULATORS
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01-NOV-1995
10-OCT-2003
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P45949;
                                                                                                                                                                                                                                                                                                         Ross P.R.;
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ARSR_BACSU
BEERE
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED furstration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 QLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 QIEKILSDETRVKIVYALLITENELCVCDLANIVEATVAATSHHIRFLKKQGIANYRKDGK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cadmium efflux system accessory protein (Cadmium resistance regulatory
              MEDLINE=94245633; PubMed=8188605;
Lebrun M., Audurier A., Cossart P.;
"Plasmid-borne cadmium resistance genes in Listeria monocytogenes are
similar to cadA and cadC of Staphylococcus aureus and are induced by
cadmium.";
                                                                                                                             STRAIN-LM74; TRANSPOSON-TD542;

MEDLINE-94245634; PubMed=8188606;
Lebrun M., Audurier A., Cossart P.;

"Plasmid-borne cadmium resistance genes in Listeria monocytogenes are present on TD5422, a novel transposon closely related to TD917.";

J. Bacteriol. 176:3049-3061(1994).

-! FUNCTION: Not yet known.

-! SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR01045; HTH ArsR.
Pfam; PF01022; HTH 5; 1.
PRINTS; PR00778; HTHARSR.
SWART; SM00418; HTHARSR.
PROSITE; PS00846; HTH ARSR. FAMILY; 1.
Transcription regulation; DNA-binding; Cadmium resistance; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=L.innocua; STRAIN-CLIP 11262 / Serovar 6a; PLASMID=pLI100; MEDLINE=21537279; PubMed=11679669; Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.7%; Score 145; DB 1; Length 119; 47.8%; Pred. No. 5.7e-09; Live 9; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactococcus lactis (subsp. lactis) (Streptococcus lactis) Plasmid pLI100, Plasmid pND302, and Plasmid pAH82.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria. NCBL_TaxID=1642, 1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 77 H-T-H MOTIF (POTENTIAL).
119 AA; 13489 MW; 040D3AC8085A4EE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 AA.
                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (sor send an email to license@isb-sib.ch)
                                                                                          J. Bacteriol. 176:3040-3048(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                           EMBL; L28104; AAA25276.1; -.
HSSP; P30340; 1SMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transposable element
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetcuani F., Couve B., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant I., Dussurget O., Entian K.-D., Faihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Therrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Novel type I restriction specificities through domain shuffling of Hads subunits in lactococcus lactis.";
Mol. Microbiol. 36:866-875(2000).
-i- FUNCTION: Not yet known.
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Pfam, PF01022, HTH 5, 1.
PRINTS, RR00778, HTHARSR.
SMART, SM00418, HTH ARSR. 1.
PROSITE, PS00846, HTH ARSR FAMILY; 1.
Iranscription regulation; DNA-binding; Cadmium resistance; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=L.1.lactis; STRAIN=DPC220; PLASMID=pAH82;
MEDLINE=20305032; PubMed=10844674;
O'Sullivan D., Twomey D.P., Coffey A., Hill C., Fitzgerald G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=L.1.lactis; STRAIN=M71; PLASMID=pND302;
Liu C.Q., Chia G.L., Dunn N.W.; "Cadmium resistance encoded by pND302 in Lactococcus lactis.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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(Rel. 32, Last sequence update)
(Rel. 42, Last annotation update)
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EMBL; U78967; AAB37344.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Science 294:849-852(2001).
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DNA BIND 58
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Y.; DNA

resistance

Arsenical

ARSR OR BSU25810

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RAMINIES 98044033; PubMed=9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Brignel S.C., Bron S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignel S.C., Bron S.,

RA Borriss R., Codani J.J., Comnerton I.F., Cummings N.J., Daniel R.A.,

Choi S.K., Codani J.J., Comnerton I.F., Cummings N.J., Daniel R.A.,

Brian K.D., Errington J., Robert C., Ferrari E., Foulger D.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

A Ghim S.Y., Glaser P., Goffeau R., Golightly E.J., Grandi G.,

RA Ghim S.Y., Kodeter P., Goffeau R., Golightly E.J., Laya M., Jones L.,

A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Karamata D., Kasahara Y., Klaerr-Blanchard M., Melon C.,

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Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

Ranto V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

Ranto V., Pohl T.M., Portetelle D., Roper M., Sadaie Y.,

Rato T., Scanlan B., Schleich S., Schroeter R., Scoffone F.,

Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

Sorokin A., Tanaka T., Tanaka T., Tarkahashi H., Takenaru K.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Tosato V., Uchlyama S., Wandenbol M., Vannier P., Winters P., Winters P., Wander E., Wedler E., Woll S.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tarkangi L.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tarkangi R., Wanbutt R., Wedler E., Wel
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato I., Takeuchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medigue C., Moszer I., Viari A., Danchin A.;
"Analysis of a Bacillus subtilis genome fragment using a co-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato I., Kobayashi Y.;
"The ars operon in the skin element of Bacillus subtilis confers resistance to arsenate and arsenite.";
J. Bacteriol. 180:1655-1661(1998).
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR FOR THE ARS OPERON.
                                                                                                                                                                STRAIN=168 / JH642;
MEDLINE=95219086; PubMed=7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi
TComplete nucleotide sequence of a skin element excised by
rearrangement during sporulation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
                                            Bacillus subtilis.
Bacteria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiology 142:3103-3111(1996).
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Gene 165:GC37-GC51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sporulation genes."
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                                                                                             NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Kobayashi Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 QKFKALADQKRLEIMYELCQRGKTCVCDLTEIFEVTQSKLSYHLKILLDANLITKETKGT
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"The cyannobacterial repressor SmtB is predominantly a dimer and binds
two Zn2+ ions per subunit.";
Biochemistry 36:15343-15348(1997).
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0
SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                         EMBL; D32216; BAA06967.1; -.
EMBL; D84422; BAA12431.1; -.
EMBL; Z99117; CAR14522.1; -.
EMBL; Z9917; CAR14522.1; -.
EMBL; BG11301; argR.
Subtilist; BG11301; argR.
FIR + FPFO; BG11301; argR.
FFAM; PR01022; HTH ArgR.
FRINTS; PR00778; HTHARSR.
FRINTS; PR00418; HTHARSR.
FROSITE; P$00846; HTH ARSR FAMILY; 1.
Arsenical resistance; Transcription regulation; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.1%; Score 127; DB 1; Length 105; 37.3%; Pred. No. 4.6e-07; rative 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morby A.P., Turner J.S., Huckle J.W., Robinson N.J.; "SmtB is a metal-dependent repressor of the cyanobacterial metallothionein gene smtA: identification of a Zn inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Cyanobacteria, Chroccoccales; Synechococcus.
NCBI TaxID=1140;
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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MEDLINE=93197158; Pubmed=8451191;
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hes 25; Conservative
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DNA BIND 38
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                                   REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 ILKILSDSSRLEILDLL-SCGELCACDLLEHFQFSQPTLSHHMKSLVDNELVTTRKDGNK 67
          MEDLINES PEROM N.A.

MEDLINES 92276351; PubMed=1534328;

Ji G., Silver S.;

"Regulation and expression of the arsenic resistance operon from Staphylococcus aureus plasmid pl258";

Staphylococcus aureus plasmid pl258";

J. Bacteriol. 174:3664-3664(1992).

-I- FUNCTION: TRANSCRIPTIONAL REPRESSOR FOR THE ARS OPERON. ARSR IS A TRANS-ACTING MEGOLIARORY PROTEIN WHICH CONTROLS ITS OWN EXPRESSION. THE REPRESSIVE BFFECT OF ARSR IS ALLEVIANED BY OXIONS OF +III OXIDATION STATE OF ARSENIC, ANTIMONY, AND BISMUTH, AS WELL AS ARSENATE (AS (V)).

-I- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenstein R., Peschel A., Wieland B., Goetz F.;
"Expression and regulation of the antimonite, arsenite, and arsenate
"Expression and regulation of the antimonite, arsenite, and arsenate
resistance operon of Staphylococcus xylosus plasmid pSX267.";
J. Bacteriol. 174:33676-3683(1992).
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR FOR THE ARS OPERON. ARSR IS
EXPRESSION. THE REPRESSIVE BFFECT OF ARSR IS ALLEVIATED BY OXYIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 LFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRKQGKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0778; HTHARSR.
WART; SW0418; HTH ARSR.
PROSITE; PS0046; HTHARSR_FAMINY; 1.
Plasmid; Arsenical resistance; Transcription regulation; Repressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.0%; Score 111.5; DB 1; Length 104; 40.9%; Pred. No. 2.2e-05; tive 11; Mismatches 27; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA BIND 32 51 H-T-H MOTIF (POTENTIAL). SEQUENCE 104 AA; 11863 MW; 975664A2469CC417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quizzo, Charles (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-JIL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arsenical resistance operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DSM 20267 / Isolate C2A;
MEDLINE=92276350; PubMed=1534327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P30340; ISMT.
InterPro; IPR001845; HTH ArsR.
Pfam; PF01022; HTH 5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M86824; AAA25636.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B41903; B41903.
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68 HWYQLN 73
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[1]
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

MEDLINE=98128797; PubMed=9466913;

GOOK W.J., Kar S.R., Taylor K.B., Hall L.M.;

"Crystal structure of the cyanobacterial metallothionein repressor SmtB: a model for metalloregulatory proteins.";

J. Mol. Biol. 275:337-346(1998).

-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF THE EXPRESSION OF THE SMTA GENE. THE COMPLEX OF DNA AND SMTB IS DISASSOCIATED BY ZINC IONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 122;
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBL_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FBB-1995 (Rel. 31, Last annotation update)
Arsenical resistance operon repressor.
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27; Conservative
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97
105
122 AA;
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P30338;
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Matches 27,
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MEDLINE=92041677; PubMed=1938959;
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les 27; Conservative
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TIGR; VC0678; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S37313; S37313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFYTLS 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ILKVLSDPSRLEILDLI-SCGELCACDLLEHFQFSQPTLSHHMKSLVDNELVTTRKNGNK 67
   +III OXIDATION STATE OF ARSENIC, ANTIMONY, AND BISMUTH, AS WELL
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"A functional homolog of Escherichia coli NhaR in Vibrio cholerae.";
J. Bacteriol. 180:762-765(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00418; HTH ARSK; 1.
PROSITE; PS00846; HTH ARSR FAMILY; 1.
Plasmid; Arsenical resistance; Transcription regulation; Repressor;
DNA-binding. 32 51 H-T-H MOTIF (POTENTIAL).
DNA_BIND 32 51 H-T-H MOTIF (POTENTIAL).
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STRAIN=El Tor N16961 / Serotype Ol;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDILINE=94049116; PubMed=8231807;
Williams S.G., Attridge S.R., Manning P.A.;
Williams S.G., Attridge S.R., Manning P.A.;
Sequence and role in virulence gene expression.";
Microbiol. 9:751-760(1993).
OF +III OXIDATION STATE OF ARSENIC, ANTIMUMI, AND BEGINELLA AS ARSENATE (AS(V)).
SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  782695; 09JMP9; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
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STRAIN=El Tor O17 / Serotype O1;
MEDLINE=98117066; PubMed=9457888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcriptional activator hlyU HLYU OR VC0678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P30340; 1SMT.
InterPro; IPR001845; HTH_ArsR.
Pfam; PF01022; HTH_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M80565; AAA27587.1; -. PIR; A41902; A41902.
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SMART; SM00418; HTH ARSR; 1.
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AC P5.5695, O9UR
DT 01-0CT-1996
DT 01-0CT-1996
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DE Transcriptio
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Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                          Nature 406:477-483 (2000).
-!- FUNCTION: UPREGUATES THE EXPRESSION OF THE HEMOLYSIN GENE, HLYA,
AND MAY PROMOTE EXPRESSION OF OTHER VINULENCE DETERMINANTS IN
VIVO. IT MAY HAVE BOTH POSITIVE AND NEGATIVE REGULATOR ACTIVITIES.
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
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SMART; SM00418; HTHARSR; 1.
Transcription regulation; Activator; DNA-binding; Complete proteome.
Transcription regulation; Activator; DNA-binding; Complete proteome.
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Nucifora G., Chu L., Misra T.K., Silver S.;
"Cadmium resistance from Staphylococous aureus plasmid p1258 cadA gene results from a cadmium-efflux ATPase.";
Proc. Natl. Acad. Sci. U.S.A. 86:3544-3548(1989).
                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Last Sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cadmium efflux system accessory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ002395; CAA05372.1; -. EMBL; AE004154; AAF93843.1; -.
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Pfam; PF01022; HTH 5; 1.
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EMBL; M90750; AAA22857.1;
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SMTB_SYNY3
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"The cadC gene product of alkaliphilic Bacillus firmus OF4 partially
restores Na+ resistance to an Escherichia coli strain lacking an
Na+/H+ antiporter (MhaA).",
J. Bacteriol. 174:4878-4884(1992).
-!- FUNCTION: Not yet known.
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J04551; AABS9153.1; -.

PIR; B32561; B32561.

HSSP; P30340; 1SMT.

PITCPPC) IPRO1022; HTH ARB.

PRINTS; PR00778; HTHARSR.

SMART; SMO418; HTH ARSR; 1.

PROSTTE; PS00846; HTH ARSR; FAMILY; 1.

Transcription regulation; DNA-binding; Cadmium resistance; Plasmid.

DNA_BIND 59 78 H-TH MOTIF (POTENTIAL).
                                Staphylococcus aureus cadA cadmium resistance
Yoon K.P., Silver S.;
"A second gene in the Staphylococcus aureus cadA cadmium resis determinant of plasmid pl258.";
J. Bacteriol. 173:7636-7642(1991).
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 21.4%; Score 108.5; DB 1; Length :
1 Similarity 38.0%; Pred. No. 5.7e-05;
27; Conservative 10; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Firmicutes; Bacillales; Bacillaceae; Bacillus.
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01-APR-1993 (Rel. 25, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AA; 13779 MW;
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NCBI_TaxID=79885;
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P30339;
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BACPF
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                                                                                                                                                                                                                                                                                                               Gaps
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Thelwell C., Robinson N.J., Turner-Cavet J.S.;
"An SmtB-like repressor from Synechocystis PCC 6803 regulates a zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-96127529; PubMed=8590279;

Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,

Sugiura M., Tabata S.;

"Sequence analysis of the genome of the unicellular cyanobacterium
"Sequence analysis of the genome of the genome.";

"Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 95:10728-10733(1998).
-!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF THE EXPRESSION OF THE
                                                                                                                                                                                                                                               1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBDATT: Homodimer (By similarity).
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
                                                                                                                                                                                                       DB 1; Length 122;
                                                       PRINTS; PRO0718; HTHARSR.
SMART; SM00418; HTH ARSR; 1.
PROSITE; PS00846; HTH ARSR FAMILY; 1.
Transcription regulation; DNA-binding; Cadmium resistance.
DNA BIND SP 78 78 HTH MOTIF (POTENTIAL).
SEQUENCE 122 AA; 13979 MW; C2FFCACFC54C8B7C CRC64;
                                                                                                                                                                                                                                               34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                     Query Match 21.2%; Score 107.5; DB 1
Best Local Similarity 36.6%; Pred. No. 7.3e-05;
Matches 26; Conservative 10; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 AA
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SMTB OR ZIAR OR SLL0792.
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HSSP; P30340; ISMT.
InterPro; IPR001845; HTH ArgR.
Pfam; PF01022; HTH 5; 1.
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HSSP, P30340; LSMT.
InterPro; IPR001845; HTH ArsR.
Pfam; PF01022; HTH_5; 1.
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SMART; SM00418; HTHARSR; 1.
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PROSITE; PS00846; HTH ARSR FAMILY; 1.
Transcription regulation; Repressor; DNA-binding; Complete proteome.
DNA BIND 72 91 H-T-H MOTIF (POTENTIAL).
SRQÜENCE 132 AA; 15083 MW; 08A7B19849B186C9 CRC64;
       S F T S
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4; Gaps Query Match 20.9%; Score 106; DB 1; Length 132; Best Local Similarity 30.7%; Pred. No. 0.00012; Matches 27; Conservative 21; Mismatches 36; Indels

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Search completed: June 2, 2004, 19:37:23 Job time: 19 secs

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June 2, 2004, 19:34:26; Search time 39 Seconds (without alignments) 784.750 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O9kii5 klebsiella	08x5d0 escherichia	O7uaw0 shigella fl	Oszbrl versinia pe	091335 Berratia ma	P74986 versinia en	08qqh7 enterobacte	0891dl pseudomonas	Ogenus pseudomonas	0881kl pseudomonas	09ili7 pseudomonas	O68020 pseudomonas	087kk6 vibrio nara	08d518 vibrio viln	O8eid5 shewanella	O8dd70 vibrio viln
SUMMARIES	ID	Q9KJI5	08X500	Q7UAW0	OBZBR1	Q9L335	P74986	Q8GGH7	Q88JD1	Q9EUUS	Q88LK1	Q911J7	068020	Q87KK6	Qadsla	OSEJDS	Q8DD70
	DB	7	16	16	16	7	7	N	16	7	16	16	7	16	16	16	16
	Query Match Length DB	116	117	114	113	106	117	106	115	118	128	116	118	111	115	114	111
æ	Query	87.7	83.6	81.2	78.9	67.6	67.2	67.0	55.7	53.4	53.0	52.6	52.4	51.2	48.8	47.8	47.3
	Score	444	423	411	399	342	340	333	282	270	268	266	265	259	247	242	239.5
	Result No.	ч	7	m	4	ហ	9	7	60	6	10	11	12	13	14	15	16

Q9kt37 vibrio chol Q8put5 methanosarc O26985 methanobact O67394 aquifex aeo O50591 acidiphiliu Q7u826 synechococc Q8ytf1 anabaena sp Q9ra93 sinorhizobi Q7v6x9 prochloroco Q820y9 streptomyce P73808 synechocyst Q7v1y1 prochloroco Q91220 streptomyce P71941 mycobacteri Q7v56 mycobacteri Q7v56 mycobacteri Q7x96 sulchonococ Q9888 streptomyce Q9888 streptomyc	Q97tj8 clostridium Q7va87 prochloroco Q8etd6 oceanobacil Q82r21 streptomyce Q9x093 thermotoga P96677 bacillus su
Q9KH37 Q26PH5 Q26PH5 Q26P394 Q50591 Q9TH21 Q9TH21 Q9TQX9 Q9TQX9 Q9TQX9 Q9TQX9 Q9TQX9 Q9TQX Q9TQX Q9X8X8 Q9X8X8 Q9X8X8 Q9X8X8 Q9X8X8 Q9X8X8 Q9X8X8 Q9X8X8	Q97TJ8 Q7VA87 Q8ETD6 Q82R21 Q9X093 P96677
	110000 110000 110000
11126 1220 1220 1220 1220 1220 1220 1220	135 103 100 98 108
4 W W W W W W W W W W W W W W W W W W W	24.0 27.5 27.5 27.2 27.2
228 182 182 173 173 166.5 165.5 165.5 165.5 165.5 153.5 153.5 151.5 151.1 147.5 147.5 147.5	141.5 139.5 139.5 137.5 137.5
11 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 4 4 4 0 11 57 56 4 12

ALIGNMENTS

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AA;
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                                                                                                                                                                                                                                     Shigella flexneri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yersinia pestis
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=623;
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                                                                             Q7UAWO;
                                                 Q7UAW0
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RESULT 3
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                              O7UAW0
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STRAIN-C157.H7 / RIMD 0509952;

MEDLINE-21156231; PubMed=112589796;

Hayashi T., Makino K., Ohnabii M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";

EMBL; AB005575; AAG58633.1; -.

EMBL; AP002565; RAB37796.1; -.
                              LQLTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LLPIQLFKILADETRLGIVLLLSELGELCVCDLCTALDQSQPKISRHLALLRESGLLLDR
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SEQUENCE FROM N.A.

MEDLINE=21074935, PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grotbeck E.J., Backett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPRO1845; HTH_ArsR.
Pfam; PF01022; HTH_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                Transcriptional repressor of chromosomal ars operon.
RASR OR 24903 OR ECS4373.
Escherichia coli 0157:#7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 423; DB 16; L
Pred. No. 6.1e-41;
                                                                                                                         61 DPKQGKWVHYRLSPQIPSWAAQVIELAWLSQQDDVQ 96
                                                                                                   97
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                                                                                                DRKOGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ
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PROSITE; PS00846; HTH ARSR FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last seq 01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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84.0%;
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Matches 79; Conservative
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                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; E86021; E86021.
PIR; E91175; E91175.
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SEQUENCE FROM N.A.
STRAIN-EKIMS / Biovar Mediaevalis;
MEDLINE-22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
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MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin M., Holzoyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Versinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arsenical resistance operon repressor (Transcriptional repressor of
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=2259024; PubMed=12704152; Menkatesan M.M., Deng W.,

MEDIINE=22590274; PubMed=12704152; Menkatesan M.M., Deng W.,

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Wei J., Goldberg M.B., Perna M.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Roumier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

Man B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

"Complete genome sequence and comparative genomics of Shigella

"Ileaneri serotype 2a strain 2457".";

Infect. Immun. 71:2775-2786(2003).

EMBL; AE016992; AAP19194.1;
                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12919 MW; 93EF861BC9C239D1 CRC64;
                                                                                                                         Transcriptional repressor of chromosomal ars operon ARSR OR S4232.
                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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     114 AA
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PRELIMINARY;
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ARSR OR YPO3346 OR Y0845.
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Gaps

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Indels

13;

22; Mismatches

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59; Conservative
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    Matches
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Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R. Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ryan D.J.;
Theeis (1999), Environmental Research Unit, Microbiology Department,.
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                        Gaps
                                                                           PIR; M0406; AD0406.

PIR; M04066; AD0406.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0006118; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR001345; YtC heme BS.

InterPro; IPR001845; HTH_ArbR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
INTEPERO; IPRO01845; HTH_ARBR.
PFam; PF01022; HTH 5; 1.
PRNINTS; PR00778; HTHARSR.
SMART; SM00418; HTHARSR; 1.
PROSITE; PS00846; HTH ARSR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Serratia.
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                                                                                                                                                                                                                      113 AA; 12821 MW; A002AFC1B9379FB1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                            78.9%; Score 399; DB 16; 76.0%; Pred. No. 3.5e-38; iive 13; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                    61 LDRKQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDV 96
                                                                                                                                                                                                                                                                                                                                                                                                                       106 AA
                                "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
EMBL; AJ414156; CAC92576.1; -.
EMBL; AE013687; AAM84430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                  PRINTS; PR00778; HTHARSR.
PROSITE; PS00190; CYTOCHROME_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ288983; CAB88406.1; -. HSSP; P30340; 1SMT.
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArsR regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kyan D.J.;
Submitted (APR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serratia marcescens.
Plasmid R478.
                                                                                                                                                             InterPro; IPR001849
Pfam; PF01022; HTH
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBL_TaxID=615;
                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ryan D.J
                                                                                                                                                                                                                                                          Local
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Matches
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Score 342; DB 2; Length 106; Pred. No. 1.2e-31;

67.6%;

Query Match Best Local Similarity

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                                 2 LQPVQLFKLLADETRSTIVMLLRESGEMCVCDICAATAQSQPKISRHMALLREAELVIDR
4 LTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LTPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR01845; HTH—ArsR.
PF01022; HTH 5; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.2%; Score 340; DB 2; Length 117; Best Local Similarity 69.8%; Pred. No. 2.3e-31; Matches 60; Conservative 15; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PRO0778; HTHARSR.
SMART; SM00418; HTH ARSR; 1.
PROSITE; PSO0646; HTH ARSR_FAMILY; 1.
DNA-binding; Plasmid.
SEQUENCE 117 AA; 13559 MW; CFB14B3BD3E47891 CRC64;
                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Arsenite inducible repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-439-80; TRANSPOSON=TN2502;
MEDLINE=97128651; PubMed=9066011;
Meyt C., Irlarte M., Thi V.H., Cornelis G.R.;
"Virulence and arsenic resistance in Yersiniae.";
J. Bacteriol. 179:612-619(1997).
                                                                                                                                   62 REGKWVHYRLSPHMPAWAAGIIDTAWNCERENIR 95
                                                                                                       64 KQGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
                                                                                                                                                                                                                                                                                                   117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 REGKWVHYRLSPHMPAWAAETITTSW 87
                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; US8366; AAB42205.1; -
EMBL; AF102990; AAD16860.1; -
HSSP; P30340; ISMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fersinia enterocolitica.
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ID QE
AC QE
DT 01
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13113 MW; B66F9603771FC6C6 CRC64;
      115 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                01-MAR-2001
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01-JUN-2003
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SEQUENCE 1
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      SEQUENCE
                                      Query Match
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                                                                                                                                                                                                                                                                                29EUUS
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                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LHPIQLFKTLSDETRLSIVMLLREAGELCVCDLCSATWEPQPKVSRHMALIREAGLVIDR 61
                                                                                                                             N [1]

N [2]

Das S., Lehn N., Arnold M., Linde H.-J.;

RI "Ars operon of Enterobacter cloacae.";

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

BRBL, AFS1304, AAO16021.1, -

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.

DR GO; GO:000322; P:regulation of transcription, DNA-dependent; IEA.

DR Fam; PF01022; HTH ArsR.

DR PKINTS; PR00778; HTHARSR.

DR SWART; SM00418; HTH ARSR; 1.

The PRINTS IN SM0418; HTHARSR; I.

The SWART; SM0418; HTHARSR; II.

The SWART; SM0418; III.

The SWART; SWART; SW0418; III.
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Utterback T., Rizzon M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001945; HTH ArsR.
Pfam; PF01022; HTH 5; II.
PRINTS; PR00778; HTHSR.
                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808 (2002).

EMBL; AE016784; AAN68326.1; -- TIGR; PP2718; --
                                                                                                                                                                                                                                                                                                                                                                         67.0%; Score 339; DB 2; Length 10
65.1%; Pred. No. 2.7e-31;
ive 21; Mismatches 9; Indels
   01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Putative arsenic-efflux pump regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ARSR-2 OR PP2718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 KOGKWVHYRLSPHIPSWAAQIIEQAW 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida (strain KT2440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                                                                           56; Conservative
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(TremBLrel.
                                                                 Enterobacter cloacae.
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Best Local Similarity
Matches 56; Conserv
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                                                                                                               NCBI_TaxID=550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             de Ferra F., Pedrazzoli E.; "Optimization of the performance of chloroaromatic degradating strains : contruction of heavy metal registancegene cassettes for Pseudomonas
                                                                                                                                     2 ITPPDVFKSLSDETRARATLIASLGELCVCELMCALNDSQPKISRHLAQLRSNGMLLDR
                                                                                                    4 LIPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
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                                                         Gaps
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GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR01845; HTH_ArsR.

Pfam; PF01022; HTH_5; 1.
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strains.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL REGULATORS.
     Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.4%; Score 270; DB 2; Length 118; 51.0%; Pred. No. 2.7e-23; Live 17; Mismatches 24; Indels
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arsenic resistance transcriptional regulator.
ARSR-1 OR PP1930.
Pseudomonas putida (strain KT2440).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                      18;
55.7%; Score 282; DB 16; 54.3%; Pred. No. 1.1e-24;
                                                                                                                                                                                                         64 KOGKWVHYRLSPHIPSWAAQIIE-----QAWLS 91
                                                                                                                                                                                                                                       118 AA
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                                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 16, Created) (TrEMBLrel. 16, Last seq (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arsenic resistance operon regulator
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                        Local Similarity 54.3
nes 51; Conservative
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HSSP; P30340; ISMT.
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Best Local Similarity
Matches 46; Conserv
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                                                                                                                              Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LIPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAINSATCC 15692 / PAO1;

STRAINSATCC 15692 / PAO1;

STRAINSATCC 15692 / PAO1;

SCOVER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                   MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nartins dos Santos V.A.P. Fouts D.E. Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White C., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Eraser C.M.; Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                             TIGR; PP1930; -. Golden, T. C. Company of Golden, T. C. C. Contracellular; IEA.

GO; GO:0005350; F:transcription factor activity; IEA.

GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR01845; HTH_ArsR.

Pfam; PF01022; HTH_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                     53.0%; Score 268; DB 16; Length 128; 54.3%; Pred. No. 5e-23; ive 17; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                         "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808 (2002).

EMBL; AE016781; AAN67547.1; -.
                                                                                                                                                                                                                                                                                                                                                           128 AA; 14487 MW; 29A5C5AA11532BC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 KQGKWVHYRLSPHIPSWAAQIIE-----QAWLS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 AA.
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HSSP, P30340, 1SMT.
GO, GO:0005622; C:intracellular, IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
 Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATORS.
EMBL; AE004653; AAG05665.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                PRINTS; PR00778; HTHARSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
Les 51; Conserv
Pseudomonadaceae;
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                                                                                                Complete proteome.
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ARSR OR PA2277
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                        3 SPAEVFKCLADETRVRATLLIVDQGELCVCELMCALADSQPKISRHLAQLRSAGLLLDRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 TPLQLFKNLSDBTRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDRK 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cai J., Salmon K., DuBow M.S.;
"A chromosomal ars operon homologue of Pseudomonas aeruginosa confers
increased resistance to arsenic and antimony in Escherichia coli.";
Microbiology 144:2705-2713(1998).
-1- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001845; HTH ArsR.
Pfam; PF01022; HTH 5; 1.
Pfam; PF01022; HTH 5; 1.
SMATY; SN00418; HTHARSR.
SMART; SN00418; HTH ARSR; 1.
DNA-binding; Transcription regulation; Complete protecme.
SEQUENCE 116 AA; 13045 MM; 3DDD19DC18F7091E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000375; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001845; HTH_ArsR.
PF01022; HTH_5; HTH_ArsR.
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Pseudomonadaceae, Pseudomonas.
                                                                                                                                                                                                                                                                   52.6%; Score 266; DB 16; Length 116; 51.6%; Pred. No. 7.7e-23; ive 22; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 118;
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l Similarity 56.1%; Pred. No. 1e-22;
46; Conservative 20; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 AA; 13049 MW; 23EDAF846A58D52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 QGQWVYYRLNPALPAWIHEVLQVTLRANGDWLQ 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 QGKWVHYRLSPHIPSWAAQIIEQAWLSQQDDVQ 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99018820; PubMed=9802012;
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SMART; SM00418; HTH ARSR; 1.
DNA-binding.
                                                                                                                                                                                                                                                                                               Local Similarity 51.69
nes 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
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Q87KK6
ID Q87KK
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PRINTS; PR00778; HTHARSR.
                                                                                                                                                                                                                                                                                                                                                    ARSR OR SO0532.
Shewanella oneidensis.
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Matches 41: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=70863;
                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                               SEQUENCE FROM N.A.

STRAIN=RIMD 2210633 / Serotype O3:K6;

MEDLINE=22508454; PubMed=126260739;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Rubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Vibrio vulnificus CMCP6.";
"Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016811; AA007813.1;
GO; GO:0005522; C:intracellular; IEA.
GO; GO:0005351; F:sugar porter activity; IEA.
GO; GO:0003700; P:transcription factor activity; IEA.
GO; GO:000481; P:trenscription factor activity; IEA.
GO; GO:0005355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001345; HPF_SerP S.
InterPro; IPR001345; HPF_AERP.
PFam; PF01022; HTH_5; 1.
                                                                                                                                                                                                                                             EMBL; AP005083; BAC61224.1; -. GO; GO:0005622; C:intracellular; IEA. GO; GO:0003700; F:transcription factor activity; IEA. GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. InterPro; IPR001845; HTH ArsR.
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                                                                                                                                                                                                                                                                                                                                                                                          Length 111;
                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                26; Indels
                                                                                                                                                                                                                                                                                                                                                               111 AA; 12910 MW; 8CA274F49C46C9C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 KOGKWVHYRLSPHIPSWAAQIIEQAWLSQ-----QDDV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      51.2%; Score 259; DB 16; 50.5%; Pred. No. 4.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 AA
                                                Transcriptional regulator, ArsR family.
                                                                                                                                                                                                                                                                                                                          PRINTS; PR00778; HTHARSR.
PROSITE; PS00846; HTHARSR_FAMILY; 1.
          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Predicted transcriptional regulator
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Best Local Similarity 50.5.
-hes 50; Conservative
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                                                                      Vibrio parahaemolyticus.
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                                                                                                                                                                                                                                                                                                                                                   Complete proteome
                                                                                                           NCBI_TaxID=670;
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01-OCT-2003
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Q8D5L8
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MEDLINE-22297686; PubMed=12368813;
Medidlberg J.F., Paulagen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Snith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 LIPLQLFKNLSDETRLGIVLLLREMGELCVCDLCMALDQSQPKISRHLAMLRESGILLDR
                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                  Length 115;
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                                                                                                                                                                                                                     Indels
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                                                                                                             115 AA; 13323 MW; E5860D534BA5232B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 AA; 13081 MW; 9BF31CA369D92CF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                             Query Match
48.8%; Score 247; DB 16;
3est Local Similarity 53.1%; Pred. No. 1.2e-20;
4atches 43; Conservative 21; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.8%; Score 242; DB 16; 50.0%; Pred. No. 4.4e-20; ative 21; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 AA
SWART; SMO0418; HTH ARSR; 1.
PROSITE; PSO0846; HTH ARSR FAMILY; 1.
PROSITE; PSO0589; PTS HPR SER; 1.
SEQUENCE 115 AA, 13323 MW; ES860DS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arsenical resistence operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 KOGKWVHYRLSPHIPSWAAQII 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RÓGOWVFYRINAELSPWCQÓVL 82
                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                              | | | | | : | : | | : : | 64 GKWVYYQIHPQLAPWMKQVLQ 84
                                                                                                                                                                                                                                                                                                                                                                                  66 GKWVHYRLSPHIPSWAAQIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alteromonadaceae; Shewanella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00778; HTHARSR.
SMART; SM00418; HTH_ARSR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Search completed: June 2, 2004, 19:38:15 Job time : 41 secs